



SEQUENCE LISTING

<110> Roche Diagnostics GmbH

<120> Method for producing an active heterodimeric AMV-RT in prokaryotic cells

<130> 5272/00/

<140>

<141>

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 1

gatgactgga attcatgact gttgcgctac atctggct

38

<210> 2

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 2

gatgactgct gcagttatta tgcaaaaaga gggctcgctt

40

<210> 3

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3

gatgactgct gcagttatta atacgcttga aaggtggctt g

41

<210> 4

<211> 1716

<212> DNA

<213> Avian Myeloblastosis Virus

<400> 4

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gaattacagt taggacatat agaaccttca cttagttgct ggaacacacc tgtctttgtg 180

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<210> 5

<211> 2574

<212> DNA

<213> Avian Myeloblastosis Virus

<400> 5

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<210> 6

<211> 572

<212> PRT

<213> Avian Myeloblastosis Virus

<400> 6

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Thr Pro Val Trp Ile Asp Gln Trp Pro Leu Pro Glu Gly Lys Leu Val
 20 25 30

Ala Leu Thr Gln Leu Val Glu Lys Glu Leu Gln Leu Gly His Ile Glu
 35 40 45

Pro Ser Leu Ser Cys Trp Asn Thr Pro Val Phe Val Ile Arg Lys Ala
 50 55 60

Ser Gly Ser Tyr Arg Leu Leu His Asp Leu Arg Ala Val Asn Ala Lys
 65 70 75 80

Leu Val Pro Phe Gly Ala Val Gln Gln Gly Ala Pro Val Leu Ser Ala
 85 90 95

Leu Pro Arg Gly Trp Pro Leu Met Val Leu Asp Leu Lys Asp Cys Phe
 100 105 110

Phe Ser Ile Pro Leu Ala Glu Gln Asp Arg Glu Ala Phe Ala Phe Thr
 115 120 125

Leu Pro Ser Val Asn Asn Gln Ala Pro Ala Arg Arg Phe Gln Trp Lys
 130 135 140

Val Leu Pro Gln Gly Met Thr Cys Ser Pro Thr Ile Cys Gln Leu Ile
 145 150 155 160

Val Gly Gln Ile Leu Glu Pro Leu Arg Leu Lys His Pro Ser Leu Arg

165 170 175

Met Leu His Tyr Met Asp Asp Leu Leu Leu Ala Ala Ser Ser His Asp
180 185 190

Gly Leu Glu Ala Ala Gly Glu Glu Val Ile Ser Thr Leu Glu Arg Ala
195 200 205

Gly Phe Thr Ile Ser Pro Asp Lys Val Gln Arg Glu Pro Gly Val Gln
210 215 220

Tyr Leu Gly Tyr Lys Leu Gly Ser Thr Tyr Val Ala Pro Val Gly Leu
225 230 235 240

Val Ala Glu Pro Arg Ile Ala Thr Leu Trp Asp Val Gln Lys Leu Val
245 250 255

Gly Ser Leu Gln Trp Leu Arg Pro Ala Leu Gly Ile Pro Pro Arg Leu
260 265 270

Met Gly Pro Phe Tyr Glu Gln Leu Arg Gly Ser Asp Pro Asn Glu Ala
275 280 285

Arg Glu Trp Asn Leu Asp Met Lys Met Ala Trp Arg Glu Ile Val Gln
290 295 300

Leu Ser Thr Thr Ala Ala Leu Glu Arg Trp Asp Pro Ala Leu Pro Leu
305 310 315 320

Glu Gly Ala Val Ala Arg Cys Glu Gln Gly Ala Ile Gly Val Leu Gly
325 330 335

Gln Gly Leu Ser Thr His Pro Arg Pro Cys Leu Trp Leu Phe Ser Thr
340 345 350

Gln Pro Thr Lys Ala Phe Thr Ala Trp Leu Glu Val Leu Thr Leu Leu
355 360 365

Ile Thr Lys Leu Arg Ala Ser Ala Val Arg Thr Phe Gly Lys Glu Val
370 375 380

Asp Ile Leu Leu Leu Pro Ala Cys Phe Arg Glu Asp Leu Pro Leu Pro
385 390 395 400

Glu Gly Ile Leu Leu Ala Leu Arg Gly Phe Ala Gly Lys Ile Arg Ser
405 410 415

Ser Asp Thr Pro Ser Ile Phe Asp Ile Ala Arg Pro Leu His Val Ser
420 425 430

Leu Lys Val Arg Val Thr Asp His Pro Val Pro Gly Pro Thr Val Phe
435 440 445

Thr Asp Ala Ser Ser Ser Thr His Lys Gly Val Val Val Trp Arg Glu
450 455 460

Gly Pro Arg Trp Glu Ile Lys Glu Ile Ala Asp Leu Gly Ala Ser Val

465 470 475 480
 Gln Gln Leu Glu Ala Arg Ala Val Ala Met Ala Leu Leu Leu Trp Pro
 485 490 495
 Thr Thr Pro Thr Asn Val Val Thr Asp Ser Ala Phe Val Ala Lys Met
 500 505 510
 Leu Leu Lys Met Gly Gln Glu Gly Val Pro Ser Thr Ala Ala Ala Phe
 515 520 525
 Ile Leu Glu Asp Ala Leu Ser Gln Arg Ser Ala Met Ala Ala Val Leu
 530 535 540
 His Val Arg Ser His Ser Glu Val Pro Gly Phe Phe Thr Glu Gly Asn
 545 550 555 560
 Asp Val Ala Asp Ser Gln Ala Thr Phe Gln Ala Tyr
 565 570

 <210> 7
 <211> 858
 <212> PRT
 <213> Avian Myeloblastosis Virus

 <400> 7
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 Thr Pro Val Trp Ile Asp Gln Trp Pro Leu Pro Glu Gly Lys Leu Val
 20 25 30
 Ala Leu Thr Gln Leu Val Glu Lys Glu Leu Gln Leu Gly His Ile Glu
 35 40 45
 Pro Ser Leu Ser Cys Trp Asn Thr Pro Val Phe Val Ile Arg Lys Ala
 50 55 60
 Ser Gly Ser Tyr Arg Leu Leu His Asp Leu Arg Ala Val Asn Ala Lys
 65 70 75 80
 Leu Val Pro Phe Gly Ala Val Gln Gln Gly Ala Pro Val Leu Ser Ala
 85 90 95
 Leu Pro Arg Gly Trp Pro Leu Met Val Leu Asp Leu Lys Asp Cys Phe
 100 105 110
 Phe Ser Ile Pro Leu Ala Glu Gln Asp Arg Glu Ala Phe Ala Phe Thr
 115 120 125
 Leu Pro Ser Val Asn Asn Gln Ala Pro Ala Arg Arg Phe Gln Trp Lys
 130 135 140
 Val Leu Pro Gln Gly Met Thr Cys Ser Pro Thr Ile Cys Gln Leu Ile
 145 150 155 160
 Val Gly Gln Ile Leu Glu Pro Leu Arg Leu Lys His Pro Ser Leu Arg

165 170 175

Met Leu His Tyr Met Asp Asp Leu Leu Leu Ala Ala Ser Ser His Asp
180 185 190

Gly Leu Glu Ala Ala Gly Glu Glu Val Ile Ser Thr Leu Glu Arg Ala
195 200 205

Gly Phe Thr Ile Ser Pro Asp Lys Val Gln Arg Glu Pro Gly Val Gln
210 215 220

Tyr Leu Gly Tyr Lys Leu Gly Ser Thr Tyr Val Ala Pro Val Gly Leu
225 230 235 240

Val Ala Glu Pro Arg Ile Ala Thr Leu Trp Asp Val Gln Lys Leu Val
245 250 255

Gly Ser Leu Gln Trp Leu Arg Pro Ala Leu Gly Ile Pro Pro Arg Leu
260 265 270

Met Gly Pro Phe Tyr Glu Gln Leu Arg Gly Ser Asp Pro Asn Glu Ala
275 280 285

Arg Glu Trp Asn Leu Asp Met Lys Met Ala Trp Arg Glu Ile Val Gln
290 295 300

Leu Ser Thr Thr Ala Ala Leu Glu Arg Trp Asp Pro Ala Leu Pro Leu
305 310 315 320

Glu Gly Ala Val Ala Arg Cys Glu Gln Gly Ala Ile Gly Val Leu Gly
325 330 335

Gln Gly Leu Ser Thr His Pro Arg Pro Cys Leu Trp Leu Phe Ser Thr
340 345 350

Gln Pro Thr Lys Ala Phe Thr Ala Trp Leu Glu Val Leu Thr Leu Leu
355 360 365

Ile Thr Lys Leu Arg Ala Ser Ala Val Arg Thr Phe Gly Lys Glu Val
370 375 380

Asp Ile Leu Leu Leu Pro Ala Cys Phe Arg Glu Asp Leu Pro Leu Pro
385 390 395 400

Glu Gly Ile Leu Leu Ala Leu Arg Gly Phe Ala Gly Lys Ile Arg Ser
405 410 415

Ser Asp Thr Pro Ser Ile Phe Asp Ile Ala Arg Pro Leu His Val Ser
420 425 430

Leu Lys Val Arg Val Thr Asp His Pro Val Pro Gly Pro Thr Val Phe
435 440 445

Thr Asp Ala Ser Ser Ser Thr His Lys Gly Val Val Val Trp Arg Glu
450 455 460

Gly Pro Arg Trp Glu Ile Lys Glu Ile Ala Asp Leu Gly Ala Ser Val

465 470 475 480
 Gln Gln Leu Glu Ala Arg Ala Val Ala Met Ala Leu Leu Leu Trp Pro
 485 490 495
 Thr Thr Pro Thr Asn Val Val Thr Asp Ser Ala Phe Val Ala Lys Met
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 Leu Leu Lys Met Gly Gln Glu Gly Val Pro Ser Thr Ala Ala Ala Phe
 515 520 525
 Ile Leu Glu Asp Ala Leu Ser Gln Arg Ser Ala Met Ala Ala Val Leu
 530 535 540
 His Val Arg Ser His Ser Glu Val Pro Gly Phe Phe Thr Glu Gly Asn
 545 550 555 560
 Asp Val Ala Asp Ser Gln Ala Thr Phe Gln Ala Tyr Pro Leu Arg Glu
 565 570 575
 Ala Lys Asp Leu His Thr Ala Leu His Ile Gly Pro Arg Ala Leu Ser
 580 585 590
 Lys Ala Cys Asn Ile Ser Met Gln Gln Ala Arg Glu Val Val Gln Thr
 595 600 605
 Cys Pro His Cys Asn Ser Ala Pro Ala Leu Glu Ala Gly Val Asn Pro
 610 615 620
 Arg Gly Leu Gly Pro Leu Gln Ile Trp Gln Thr Asp Phe Thr Leu Glu
 625 630 635 640
 Pro Arg Met Ala Pro Arg Ser Trp Leu Ala Val Thr Val Asp Thr Ala
 645 650 655
 Ser Ser Ala Ile Val Val Thr Gln His Gly Arg Val Thr Ser Val Ala
 660 665 670
 Ala Gln His His Trp Ala Thr Ala Ile Ala Val Leu Gly Arg Pro Lys
 675 680 685
 Ala Ile Lys Thr Asp Asn Gly Ser Cys Phe Thr Ser Lys Ser Thr Arg
 690 695 700
 Glu Trp Leu Ala Arg Trp Gly Ile Ala His Thr Thr Gly Ile Pro Gly
 705 710 715 720
 Asn Ser Gln Gly Gln Ala Met Val Glu Arg Ala Asn Arg Leu Leu Lys
 725 730 735
 Asp Lys Ile Arg Val Leu Ala Glu Gly Asp Gly Phe Met Lys Arg Ile
 740 745 750
 Pro Thr Ser Lys Gln Gly Glu Leu Leu Ala Lys Ala Met Tyr Ala Leu
 755 760 765
 Asn His Phe Glu Arg Gly Glu Asn Thr Lys Thr Pro Ile Gln Lys His

770 775 780
 Trp Arg Pro Thr Val Leu Thr Glu Gly Pro Pro Val Lys Ile Arg Ile
 785 790 795 800
 Glu Thr Gly Glu Trp Glu Lys Gly Trp Asn Val Leu Val Trp Gly Arg
 805 810 815
 Gly Tyr Ala Ala Val Lys Asn Arg Asp Thr Asp Lys Val Ile Trp Val
 820 825 830
 Pro Ser Arg Lys Val Lys Pro Asp Ile Ala Gln Lys Asp Glu Val Thr
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 Lys Lys Asp Glu Ala Ser Pro Leu Phe Ala
 850 855

<210> 8
 <211> 62
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 8
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 ct 62

<210> 9
 <211> 65
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 9
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 tggct 65

<210> 10
 <211> 425
 <212> DNA
 <213> Escherichia coli

<400> 10
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 ctctt 425

<210> 11
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 11
 aaaactgcag agcagtaagc cggtcataaa a

31

<210> 12
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 12
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31

<210> 13
 <211> 2155
 <212> DNA
 <213> Escherichia coli

<400> 13
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<210> 14

<211> 3139

<212> DNA

<213> Escherichia coli

<400> 14

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gcctataccc	aggatgggtga	aactctagtt	ggtcagccgg	ctaaacgtca	ggcagtgacg	180
aacccgcaaa	acactctgtt	tgcgattaaa	cgctcgattg	gtcgccgctt	ccaggacgaa	240
gaagtacagc	gtgatgtttc	catcatgccg	ttcaaaatta	ttgctgctga	taacggcgac	300
gcatgggtcg	aagttaaagg	ccagaaaatg	gcaccgccgc	agatttctgc	tgaagtgtcg	360
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02/11/2002

VERIFICATION SUMMARY REPORT
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